

0590
0709

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/045,202

DATE: 07/11/2002

TIME: 16:11:19

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Output Set: N:\CRF3\07112002\J045202.raw

3 <110> APPLICANT: Bristol-Myers Squibb
 4 Bristol-Myers Squibb
 6 <120> TITLE OF INVENTION: MODULATORS OF BRUTON'S TYROSINE KINASE AND BRUTON'S TYROSINE
 KINASE
 7 INTERMEDIATES AND METHODS FOR THEIR IDENTIFICATION AND USE IN THE TREATMENT AND
 8 PREVENTION OF OSTEOPOROSIS AND RELATED DISEASE STATES
 10 <130> FILE REFERENCE: D0032 NP
 12 <140> CURRENT APPLICATION NUMBER: 10/045,202
 C--> 13 <141> CURRENT FILING DATE: 2002-06-27
 15 <150> PRIOR APPLICATION NUMBER: 60/242,471
 16 <151> PRIOR FILING DATE: 2000-10-23
 18 <160> NUMBER OF SEQ ID NOS: 12
 20 <170> SOFTWARE: PatentIn version 3.1
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 23 <211> LENGTH: 2560
 24 <212> TYPE: DNA
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 32 aaagaagaag ctatggccgc agtgattctg gagagcatct ttctgaagcg atcccaacag 180
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117 <212> TYPE: PRT

118 <213> ORGANISM: Human

120 <400> SEQUENCE: 2

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127 20 25 30
130 Thr Val His Lys Leu Ser Tyr Tyr Glu Tyr Asp Phe Glu Arg Gly Arg
131 35 40 45
134 Arg Gly Ser Lys Lys Gly Ser Ile Asp Val Glu Lys Ile Thr Cys Val
135 50 55 60
138 Glu Thr Val Val Pro Glu Lys Asn Pro Pro Pro Glu Arg Gln Ile Pro
139 65 70 75 80
142 Arg Arg Gly Glu Glu Ser Ser Glu Met Glu Gln Ile Ser Ile Ile Glu
143 85 90 95
146 Arg Phe Pro Tyr Pro Phe Gln Val Val Tyr Asp Glu Gly Pro Leu Tyr
147 100 105 110
150 Val Phe Ser Pro Thr Glu Glu Leu Arg Lys Arg Trp Ile His Gln Leu
151 115 120 125
154 Lys Asn Val Ile Arg Tyr Asn Ser Asp Leu Val Gln Lys Tyr His Pro
155 130 135 140
158 Cys Phe Trp Ile Asp Gly Gln Tyr Leu Cys Cys Ser Gln Thr Ala Lys
159 145 150 155 160
162 Asn Ala Met Gly Cys Gln Ile Leu Glu Asn Arg Asn Gly Ser Leu Lys
163 165 170 175
166 Pro Gly Ser Ser His Arg Lys Thr Lys Lys Pro Leu Pro Pro Thr Pro
167 180 185 190
170 Glu Glu Asp Gln Ile Leu Lys Lys Pro Leu Pro Pro Glu Pro Ala Ala
171 195 200 205
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179 225      230      235      240
182 Tyr Phe Ile Leu Glu Glu Ser Asn Leu Pro Trp Trp Arg Ala Arg Asp
183      245      250      255
186 Lys Asn Gly Gln Glu Gly Tyr Ile Pro Ser Asn Tyr Val Thr Glu Ala
187      260      265      270
190 Glu Asp Ser Ile Glu Met Tyr Glu Trp Tyr Ser Lys His Met Thr Arg
191      275      280      285
194 Ser Gln Ala Glu Gln Leu Leu Lys Gln Glu Gly Lys Glu Gly Gly Phe
195      290      295      300
198 Ile Val Arg Asp Ser Ser Lys Ala Gly Lys Tyr Thr Val Ser Val Phe
199 305      310      315      320
202 Ala Lys Ser Thr Gly Asp Pro Gln Gly Val Ile Arg His Tyr Val Val
203      325      330      335
206 Cys Ser Thr Pro Gln Ser Gln Tyr Tyr Leu Ala Glu Lys His Leu Phe
207      340      345      350
210 Ser Thr Ile Pro Glu Leu Ile Asn Tyr His Gln His Asn Ser Ala Gly
211      355      360      365
214 Leu Ile Ser Arg Leu Lys Tyr Pro Val Ser Gln Gln Asn Lys Asn Ala
215      370      375      380
218 Pro Ser Thr Ala Gly Leu Gly Tyr Gly Ser Trp Glu Ile Asp Pro Lys
219 385      390      395      400
222 Asp Leu Thr Phe Leu Lys Glu Leu Gly Thr Gly Gln Phe Gly Val Val
223      405      410      415
226 Lys Tyr Gly Lys Trp Arg Gly Gln Tyr Asp Val Ala Ile Lys Met Ile
227      420      425      430
230 Lys Glu Gly Ser Met Ser Glu Asp Glu Phe Ile Glu Glu Ala Lys Val
231      435      440      445
234 Met Met Asn Leu Ser His Glu Lys Leu Val Gln Leu Tyr Gly Val Cys
235      450      455      460
238 Thr Lys Gln Arg Pro Ile Phe Ile Ile Thr Glu Tyr Met Ala Asn Gly
239 465      470      475      480
242 Cys Leu Leu Asn Tyr Leu Arg Glu Met Arg His Arg Phe Gln Thr Gln
243      485      490      495
246 Gln Leu Leu Glu Met Cys Lys Asp Val Cys Glu Ala Met Glu Tyr Leu
247      500      505      510
250 Glu Ser Lys Gln Phe Leu His Arg Asp Leu Ala Ala Arg Asn Cys Leu
251      515      520      525
254 Val Asn Asp Gln Gly Val Val Lys Val Ser Asp Phe Gly Leu Ser Arg
255      530      535      540
258 Tyr Val Leu Asp Asp Glu Tyr Thr Ser Ser Val Gly Ser Lys Phe Pro
259 545      550      555      560
262 Val Arg Trp Ser Pro Pro Glu Val Leu Met Tyr Ser Lys Phe Ser Ser
263      565      570      575
266 Lys Ser Asp Ile Trp Ala Phe Gly Val Leu Met Trp Glu Ile Tyr Ser
267      580      585      590
270 Leu Gly Lys Met Pro Tyr Glu Arg Phe Thr Asn Ser Glu Thr Ala Glu
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291 <211> LENGTH: 2468
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300 agagaggaag ccatggctgc agtgatactg gagagcatct ttctgaagcg ctcccagcag      180
302 aaaaagaaaa catcaccttt aaacttcaag aagcgccgtg ttctcttgac tgtacacaaa      240
304 ctttcatact atgaatatga ctttgaacgt gggagaagag gcagtaagaa aggttcaata      300
306 gatgttgaga agatcacctg tgttgaaaca gtaattcctg aaaaaaatcc cccaccagaa      360
308 agacagattc cgaggagagg tgaggagtct agtgaaatgg aacagatttc aatcattgaa      420
310 aggttcccggt acccattcca ggttgatat gatgaaggac ctctctatgt tttctcccca      480
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316 cagacagcca agaattgctat gggctgccaa attttggaaga acaggaatgg aagcttaaaa      660
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332 gtgtctgtgt ttgctaaatc tactggggag cctcaagggg tgatccgcca ttacgttggtg      1140
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378 gccattaa
381 <210> SEQ ID NO: 4
382 <211> LENGTH: 659
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384 <213> ORGANISM: Murine
386 <400> SEQUENCE: 4
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393 20 25 30
396 Thr Val His Lys Leu Ser Tyr Tyr Glu Tyr Asp Phe Glu Arg Gly Arg
397 35 40 45
400 Arg Gly Ser Lys Lys Gly Ser Ile Asp Val Glu Lys Ile Thr Cys Val
401 50 55 60
404 Glu Thr Val Ile Pro Glu Lys Asn Pro Pro Pro Glu Arg Gln Ile Pro
405 65 70 75 80
408 Arg Arg Gly Glu Glu Ser Ser Glu Met Glu Gln Ile Ser Ile Ile Glu
409 85 90 95
412 Arg Phe Pro Tyr Pro Phe Gln Val Val Tyr Asp Glu Gly Pro Leu Tyr
413 100 105 110
416 Val Phe Ser Pro Thr Glu Glu Leu Arg Lys Arg Trp Ile His Gln Leu
417 115 120 125
420 Lys Asn Val Ile Arg Tyr Asn Ser Asp Leu Val Gln Lys Tyr His Pro
421 130 135 140
424 Cys Phe Trp Ile Asp Gly Gln Tyr Leu Cys Cys Ser Gln Thr Ala Lys
425 145 150 155 160
428 Asn Ala Met Gly Cys Gln Ile Leu Glu Asn Arg Asn Gly Ser Leu Lys
429 165 170 175
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433 180 185 190
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441 210 215 220
444 Tyr Met Pro Met Asn Ala Asn Asp Leu Gln Leu Arg Lys Gly Glu Glu
445 225 230 235 240
448 Tyr Phe Ile Leu Glu Glu Ser Asn Leu Pro Trp Trp Arg Ala Arg Asp
449 245 250 255
452 Lys Asn Gly Gln Glu Gly Tyr Ile Pro Ser Asn Tyr Ile Thr Glu Ala
453 260 265 270
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461 290 295 300
464 Ile Val Arg Asp Ser Ser Lys Ala Gly Lys Tyr Thr Val Ser Val Phe

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RAW SEQUENCE LISTING ERROR SUMMARY
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VERIFICATION SUMMARY

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